

(FILE 'HOME' ENTERED AT 11:31:21 ON 25 SEP 2000)

INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, AIDSLINE, ANABSTR, AQUASCI,  
CABA, BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO,  
CANCERLIT, CAPLUS, CEABA, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU,  
DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 11:31:31 ON 25 SEP  
2000

SEA CARTILAGE OLIGOMERIC MATRIX PROTEIN

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10 FILE ADISALERTS  
1 FILE AGRICOLA  
1 FILE BIOCOMMERCE  
149 FILE BIOSIS  
2 FILE BIOTECHABS  
2 FILE BIOTECHDS  
69 FILE BIOTECHNO  
6 FILE CABA  
14 FILE CANCERLIT  
101 FILE CAPLUS  
3 FILE CONFSCI  
4 FILE DDFU  
47 FILE DGENE  
4 FILE DRUGU  
7 FILE EMBAL  
112 FILE EMBASE  
73 FILE ESBIODASE  
28 FILE GENBANK  
3 FILE JICST-EPLUS  
36 FILE LIFESCI  
114 FILE MEDLINE  
2 FILE PROMT  
141 FILE SCISEARCH  
6 FILE TOXLINE  
13 FILE TOXLIT  
4 FILE USPATFULL  
8 FILE WPIDS  
8 FILE WPINDEX

L1 QUE CARTILAGE OLIGOMERIC MATRIX PROTEIN

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SEA L1 AND (VARIANT? OR SPLICE)

-----  
6 FILE BIOSIS  
5 FILE BIOTECHNO  
4 FILE CAPLUS  
2 FILE EMBAL  
6 FILE EMBASE  
4 FILE ESBIODASE  
2 FILE LIFESCI  
5 FILE MEDLINE  
5 FILE SCISEARCH  
3 FILE USPATFULL

L2 QUE L1 AND (VARIANT? OR SPLICE)

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FILE 'BIOSIS, EMBASE, BIOTECHNO, MEDLINE, SCISEARCH, CAPLUS, ESBIODASE,  
USPATFULL, EMBAL, LIFESCI' ENTERED AT 11:38:50 ON 25 SEP 2000

L3 42 S L1 AND (VARIANT? OR SPLICE)

1\* FILE FSTA  
 0\* FILE KOSMET  
 0\* FILE MEDICONF  
 3 FILE MEDLINE  
 0\* FILE NTIS  
 1 FILE SCISEARCH  
 2 FILE TOXLINE  
 10 FILE USPATFULL  
 L2 QUE L1 AND (DIET OR EAT? OR INGEST?)  
 -----

FILE 'USPATFULL, BIOSIS, CABA, CAPLUS, EMBASE, MEDLINE, TOXLINE,  
 AGRICOLA, DRUGU, SCISEARCH, FSTA' ENTERED AT 07:02:03 ON 25 SEP 2000  
 L3 3315 S SOY(15W) (DIET OR EAT? OR INGEST?)  
 L4 193 S L3 AND (DIET OR EAT? OR INGEST?) (15W) LIVER  
 L5 2 S L4 AND LIVER(15W) (ENLARG? OR SWELL?)  
 L6 3 S L4 AND TRYPSIN  
 L7 3 DUP REM L6 (0 DUPLICATES REMOVED)  
 L8 5 S L3 AND SOY(15W) (ENLARG?)  
 L9 2 DUP REM L8 (3 DUPLICATES REMOVED)

INDEX 'ADISALERTS, ADISINSIGHT, AGRICOLA, AIDSLINE, ANABSTR, AQUASCI,  
 BIOBUSINESS, BIOCOMMERCE, BIOSIS, BIOTECHABS, BIOTECHDS, BIOTECHNO,  
 CABA,  
 CANCERLIT, CAPLUS, CEABA, CEN, CIN, CONFSCI, CROPB, CROPU, DDFB, DDFU,  
 DGENE, DRUGB, DRUGLAUNCH, DRUGMONOG2, ...' ENTERED AT 07:12:39 ON 25 SEP  
 2000

SEA (PROTEIN? OR PEPTIDE?) (15W) (AGGREGAT? OR OLIGOMERIZ?)  
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45 FILE ADISALERTS  
 15 FILE ADISINSIGHT  
 429 FILE AGRICOLA  
 101 FILE AIDSLINE  
 41 FILE ANABSTR  
 133 FILE AQUASCI  
 354 FILE BIOBUSINESS  
 36 FILE BIOCOMMERCE  
 8129 FILE BIOSIS  
 460 FILE BIOTECHABS  
 460 FILE BIOTECHDS  
 3317 FILE BIOTECHNO  
 907 FILE CABA  
 912 FILE CANCERLIT  
 9886 FILE CAPLUS  
 152 FILE CEABA  
 55 FILE CEN  
 33 FILE CIN  
 77 FILE CONFSCI  
 5 FILE CROPB  
 10 FILE CROPU  
 178 FILE DDFB  
 309 FILE DDFU  
 2645 FILE DGENE  
 178 FILE DRUGB  
 5 FILE DRUGNL  
 540 FILE DRUGU  
 83 FILE EMBAL  
 6750 FILE EMBASE  
 2554 FILE ESBIODASE  
 417 FILE FROSTI  
 777 FILE FSTA  
 31 FILE GENBANK  
 4 FILE HEALSAFE  
 318 FILE IFIPAT  
 366 FILE JICST-EPLUS

12 FILE KOSMET  
 2360 FILE LIFESCI  
 2 FILE MEDICONF  
 6438 FILE MEDLINE  
 37 FILE NIOSHTIC  
 72 FILE NTIS  
 25 FILE OCEAN  
 10 FILE PHAR  
 30 FILE PHIN  
 173 FILE PROMT  
 5489 FILE SCISEARCH  
 1071 FILE TOXLINE  
 1590 FILE TOXLIT  
 3132 FILE USPATFULL  
 552 FILE WPIDS  
 552 FILE WPINDEX

L10 QUE (PROTEIN? OR PEPTIDE?) (15W) (AGGREGAT? OR OLIGOMERIZ?)

FILE 'CAPLUS, BIOSIS, EMBASE, MEDLINE, SCISEARCH, BIOTECHNO, USPATFULL,  
 DGENE, ESBIODBASE, LIFESCI, TOXLIT, TOXLINE, CANCERLIT, CABA, FSTA,  
 WPIDS,  
 DRUGU, BIOTECHDS, AGRICOLA, FROSTI, JICST-EPLUS, BIOBUSINESS, IFIPAT,  
 DRUGB, PROMT, CEABA, AQUASCI, AIDSLINE, ...' ENTERED AT 07:16:39 ON 25  
 SEP 2000

L11 4850 S (PROTEIN? OR PEPTIDE?) (15W) (OLIGOMERIZ?)  
 L12 117 S L11 AND PENTA?  
 L13 61 DUP REM L12 (56 DUPLICATES REMOVED)  
 L14 35 S L12 AND SPACE?  
 L15 28 DUP REM L14 (7 DUPLICATES REMOVED)  
 L16 14 S L15 AND PROLINE

cytotoxin at pH 7.4 measured by CD- and ATR-FTIR-spectroscopy consists of about 50 % .beta.-sheet, 10 % .alpha.-helix as well as 40 % .beta.-turn and random coil. Decreasing medium pH to 6.0 does not notably influence the FTIR spectrum. But incubation with SDS results in a rise to about 70 % .beta.-structure, consisting of long, antiparallel .beta.-sheets. The detergent OPOE increases the amt. of .beta.-structure to approx. 55-60 %. The spectrum is different, but closely related to those of the isolated membrane bound monomer and the liposome assocd. monomeric and **pentameric** toxin. This leads to the conclusion that contact with detergents or lipids introduce an increase of .beta.-structure. This might expose a hydrophobic surface of the cytotoxin mol. that facilitates oligomerization as well as membrane insertion.

IT Oligomerization

Pseudomonas aeruginosa

Secondary structure (**protein**)

(**oligomerization** and structural changes of Pseudomonas aeruginosa cytotoxin)

L13 ANSWER 46 OF 61 CAPLUS COPYRIGHT 2000 ACS DUPLICATE 9

AN 1996:314952 CAPLUS

DN 125:2858

TI Sex-specific and non-sex-specific oligomerization domains in both of the doublesex transcription factors from Drosophila melanogaster

AU An, Wenqian; Cho, Sayeon; Ishii, Haruhiko; Wensink, Pieter C.

CS Department Biochemistry, Brandeis University, Waltham, MA, 02254-9110,

USA

SO Mol. Cell. Biol. (1996), 16(6), 3106-3111

CODEN: MCEBD4; ISSN: 0270-7306

DT Journal

LA English

AB The doublesex gene of Drosophila melanogaster encodes the alternatively spliced, sex-specific transcription factors DSXM and DSXF. These factors regulate male- and female-specific transcription of many genes. For example, female-specific transcription of the yolk protein 1 gene is regulated by DSXM repression in males and DSXF activation in females. In this study we used in vitro interaction assays and the in vivo yeast two-hybrid method to identify and examine oligomerization domains of the DSX proteins. A 66-amino-acid segment common to both **proteins** (amino acids 39 to 104) contains a sequence-specific DNA binding domain and an **oligomerization** domain (OD1). The OD1 domain oligomerizes up to at least a **pentamer**, but only dimers bound to a palindromic regulatory site in the yolk protein 1 gene are detected. Both subunits of the OD1 dimer are in contact with DNA. Another segment of each protein (amino acids 350 to 412 for DSXF and 350 to 427 for DSXM) contains a second oligomerization domain (OD2F and OD2M, resp.). The OD2 domains have both sex-specific and non-sex-specific sequences which are necessary for oligomerization. On the basis of sequence anal., we

predict

that OD2 oligomerizes through coiled-coil interactions. We speculate

that

the common function of OD1 and OD2 is to oligomerize the full-length proteins, whereas their specialized functions are to form a dimeric DNA binding unit and a sex-specific transcriptional activation or repression unit.

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a palindromic regulatory site in the yolk protein 1 gene are detected. Both subunits of the OD1 dimer are in contact with DNA. Another segment of each protein (amino acids 350 to 412 for DSXF and 350 to 427 for DSXM) contains a second oligomerization domain (OD2F and OD2M, resp.). The OD2 domains have both sex-specific and non-sex-specific sequences which are necessary for oligomerization. On the basis of sequence anal., we predict that OD2 oligomerizes through coiled-coil interactions. We speculate that the common function of OD1 and OD2 is to oligomerize the full-length proteins, whereas their specialized functions are to form a dimeric DNA binding unit and a sex-specific transcriptional activation or repression unit.

L13 ANSWER 47 OF 61 BIOSIS COPYRIGHT 2000 BIOSIS DUPLICATE 10  
 AN 1996:533580 BIOSIS  
 DN PREV199699255936  
 TI The crystal structure of a five-stranded coiled coil in COMP: A prototype ion channel.  
 AU Malashkevich, Vladimir N. (1); Kammerer, Richard A.; Efimov, Vladimir P.; Schulthess, Therese; Engel, Juergen  
 CS (1) Dep. Structural Biol., Biozentrum, Univ. Basel, Klingelbergstrasse 70,  
 CH-4056 Basel Switzerland  
 SO Science (Washington D C), (1996) Vol. 274, No. 5288, pp. 761-765.  
 ISSN: 0036-8075.

DT Article  
 LA English  
 AB Oligomerization by the formation of alpha-helical bundles is common in many **proteins**. The crystal structure of a parallel **pentameric** coiled coil, constituting the **oligomerization** domain in the cartilage oligomeric matrix protein (COMP), was determined at 2.05 angstroms resolution. The same structure probably occurs in two other extracellular matrix proteins, thrombospondins 3 and 4. Complementary hydrophobic interactions and conserved disulfide bridges between the alpha helices result in a thermostable structure with unusual properties. The long hydrophobic axial pore is filled with water molecules

but can also accommodate small apolar groups. An "ion trap" is formed inside the pore by a ring of conserved glutamines, which binds chloride and probably other monatomic anions. The oligomerization domain of COMP has marked similarities with proposed models of the **pentameric** transmembrane ion channels in phospholamban and the acetylcholine receptor.  
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L13 ANSWER 51 OF 61 CAPLUS COPYRIGHT 2000 ACS  
 AN 1994:403573 CAPLUS  
 DN 121:3573  
 TI Mitochondrial Mas70p signal anchor sequence. Mutations in the transmembrane domain that disrupt dimerization but not targeting or membrane insertion  
 AU Millar, Douglas G.; Shore, Gordon C.  
 CS Dep. Biochem., McGill Univ., Montreal, PQ, H3G 1Y6, Can.  
 SO J. Biol. Chem. (1994), 269(16), 12229-32  
 CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

AB Protein Mas70p is an integral membrane protein in *Saccharomyces cerevisiae*

that is targeted and inserted into the mitochondrial outer membrane in an Nin-Ccyto orientation by its N-terminal 29-amino acid signal anchor sequence. Recently, the authors demonstrated that the signal anchor was capable of mediating homo-oligomerization of a fusion protein, pOMD29, in the outer membrane in vitro. Consistent with this finding, the authors show here that a synthetic peptide corresponding to the Mas70p signal anchor is capable of independent membrane insertion and dimerization with pOMD29. To further map the oligomerization domain in the signal anchor sequence, a deletion mutant of pOMD29 that lacks amino acids 2-10 was constructed. This protein, pOMD29.DELTA.2-10, efficiently participated

in

dimer formation following import, indicating that dimerization was mediated by the putative membrane spanning segment (amino acids 11-29). This segment was predicted to form an .alpha.-helix that has an alanine-rich face and contains multiple copies of a **pentapeptide** dimerization motif that is widespread among members of the receptor tyrosine kinase family. Substitution of the alanine residues in one of these copies with isoleucine, producing a potentially bulkier contact surface, resulted in a protein which was targeted and inserted into the outer membrane but failed to assemble into dimers. Taken together, these results identify a structural feature of the signal anchor transmembrane domain that is important for oligomerization but is not required for targeting and membrane insertion.

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that is targeted and inserted into the mitochondrial outer membrane in an Nin-Ccyto orientation by its N-terminal 29-amino acid signal anchor sequence. Recently, the authors demonstrated that the signal anchor was capable of mediating homo-oligomerization of a fusion protein, pOMD29, in the outer membrane in vitro. Consistent with this finding, the authors show here that a synthetic peptide corresponding to the Mas70p signal anchor is capable of independent membrane insertion and dimerization with pOMD29. To further map the oligomerization domain in the signal anchor sequence, a deletion mutant of pOMD29 that lacks amino acids 2-10 was constructed. This protein, pOMD29.DELTA.2-10, efficiently participated

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ST mitochondria **protein Mas70p oligomerization** domain  
localization

IT Mitochondria

(**protein** Mas70p of, of *Saccharomyces cerevisiae*, localization  
of **oligomerization** region of signal anchor transmembrane  
domain of)

IT **Proteins**, specific or class

RL: BIOL (Biological study)

(MAS70 (mitochondrial assembly, 70,000-mol.-wt.), of *Saccharomyces cerevisiae*, localization of **oligomerization** region of signal  
anchor transmembrane domain of)

AN 93:24822 USPATFULL  
TI Generation and selection of novel DNA-binding proteins and polypeptides  
IN Ladner, Robert C., Ijamsville, MD, United States  
Guterman, Sonia K., Belmont, MA, United States  
Kent, Rachel B., Boxborough, MA, United States  
Ley, Arthur C., Newton, MA, United States  
PA Protein Engineering Corp., Cambridge, MA, United States (U.S.  
corporation)  
PI US 5198346 19930330  
AI US 1990-558011 19900726 (7)  
RLI Continuation-in-part of Ser. No. US 1989-293980, filed on 6 Jan 1989,  
now patented, Pat. No. US 5096815  
DT Utility  
EXNAM Primary Examiner: Lacey, David L.; Assistant Examiner: Ulm, John D.  
LREP Cooper, Iver P.  
CLMN Number of Claims: 48  
ECL Exemplary Claim: 24  
DRWN 16 Drawing Figure(s); 16 Drawing Page(s)  
LN.CNT 10332

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB Novel DNA-binding proteins, especially repressors of gene expression,  
are obtained by variegation of genes encoding known binding proteins  
and

selection for proteins binding the desired target DNA sequence. A novel  
selection vector may be used to reduce artifacts. Heterooligomeric  
proteins which bind to a target DNA sequence which need not be  
palindromic are obtained by a variety of methods, e.g., variegation to  
obtain proteins binding symmetrized forms of the half-targets and  
heterodimerization to obtain a protein binding the entire asymmetric  
target.

DETD . . . of full-length polypeptides. Thus it is preferred that the  
gene

containing the amber, ochre, or opal mutations code for a  
**protein** that acts as a monomer. Inhibition of  
**oligomerization** can also be avoided by placing the amber, ochre,  
or opal mutations very near the amino terminus of the protein. . . .

DETD The P22 Mnt repressor, like lambda Cro, is a small **protein**  
containing both DNA-binding and **oligomerization** sites. Unlike  
Cro, P22 Mnt is a tetramer in solution (VERS85b, VERS87a). The amino  
acid sequence of Mnt has been. . . .

DETD . . . as the parental DBP, but which prevents oligomerization. It is  
anticipated that reverse selection will isolate many genes for  
non-functional **proteins** and that these **proteins** must  
be analyzed until a suitable **oligomerization**-mutant is found.  
Therefore, we choose sites carefully so that we maximize the chance of  
disrupting oligomerization without destroying tertiary structure.. . .

DETD It is also possible to modulate DNA-binding specificity by altering the  
**protein-protein** interface. Because the  
**oligomerization** equilibrium is coupled to DNA binding, mutations  
that damage **oligomerization** (see discussion, supra) reduce  
operator site affinity. Since oligomerization involves the matching of  
**protein** surfaces, many interactions are hydrophobic in nature  
and mutations which specifically destabilize **oligomerization**  
are similar to mutations which destabilize global **protein**  
structure. Interactions at the site of **oligomerization** can  
influence the strength of interactions at the DNA-binding site by

subtle  
alterations in protein structure.

DETD GOFF87: Goff, S A, S R Short-Russell, and J F Dice, "Efficient  
Saturation Mutagenesis of a **Pentapeptide** Coding Sequence Using  
Mixed Oligonucleotides", DNA (1987), 6(4)381-388.

CLM What is claimed is:

. . . the host cell, and (e) forward selecting for expression from a step  
(c) variegant gene of a second oligomerization mutant **protein**

which is capable of forming a heterooligomer with said first **oligomerization** mutant protein, said heterooligomer binding said ultimate target DNA sequence, and (f) isolating the genes encoding said heterooligomer.

L13 ANSWER 53 OF 61 CAPLUS COPYRIGHT 2000 ACS

AN 1993:535215 CAPLUS

DN 119:135215

TI Membrane orientation and oligomerization of the small hydrophobic protein of human respiratory syncytial virus

AU Collins, Peter L.; Mottet, Genevieve

CS Lab. Infect. Dis., Natl. Inst. Allergy Infect. Dis., Bethesda, MD, 20892, USA

SO J. Gen. Virol. (1993), 74(7), 1445-50

CODEN: JGVIAY; ISSN: 0022-1317

DT Journal

LA English

AB Previous work has demonstrated that the small hydrophobic (SH) protein of human respiratory syncytial virus (RSV) A2 strain is a 64 amino acid integral membrane protein that accumulates intracellularly as an unglycosylated major species (SH0), a minor species truncated at the

amino

terminus and two N-glycosylated species one of which contains a further addn. of polylactosamine. In this study, the membrane orientation of SH0 was mapped by trypsinization of intact RSV-infected cells followed by washout, lysis and immunopptn. of protected fragments with antisera specific for the protein termini. This showed that the C terminus is extracellular and the SH protein was not detectably palmitylated. Anal. of the SH protein by sedimentation on sucrose gradients showed that it rapidly assembles into a homo-oligomer that co-sediments with the f protein tetramer. Interestingly, all forms of the SH protein were found in the oligomeric fraction. Chem. crosslinking generated species which appeared to represent dimers, trimers, tetramers and **pentamers** as well as a minor species of 180K which might correspond to the oligomeric form detected by sucrose gradient sedimentation.

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ST respiratory syncytial virus **protein oligomerization**

IT **Proteins**, specific or class

RL: RCT (Reactant)

(SH (small hydrophobic), of human respiratory syncytial virus,

membrane

orientation and **oligomerization** of, in infected cells)

IT Animal cell

(disease, infection, with human respiratory syncytial virus, viral small hydrophobic **protein** membrane orientation and

**oligomerization** in)

IT Virus, animal



(human respiratory syncytial, small hydrophobic **protein** of, membrane orientation and **oligomerization** of, in infected cells)

L13 ANSWER 57 OF 61 CAPLUS COPYRIGHT 2000 ACS

AN 1992:126527 CAPLUS

DN 116:126527

TI Defined chemically cross-linked oligomers of human C-reactive protein: characterization and reactivity with the complement system

AU Jiang, H.; Lint, T. F.; Gewurz, H.

CS Dep. Immunol./Microbiol., Rush Med. Coll., Chicago, IL, 60612, USA

SO Immunology (1991), 74(4), 725-31

CODEN: IMMUAM; ISSN: 0019-2805

DT Journal

LA English

AB Chem. cross-linked C-reactive protein (CRP) oligomers were prepd. and characterized, and Clq binding and complement (C) activation were investigated. Purified human CRP was polymd. in the presence of both non-cleavable and cleavable crosslinking agents and further sepd. by Superose 12 anal. FPLC column chromatog. into fractions of 110 KDa (**pentameric** monomers), 220 KDa (dimers) and 330 KDa (trimers); virtually no larger oligomers were formed under a variety of exptl. conditions. CRP subunits were cross-linked both within and between CRP **pentamers**. CRP trimers retained native CRP antigenicity without expression of neo-CRP epitopes. CRP trimers showed maximal binding and CRP dimers showed partial binding of solid phase Clq while CRP monomers bound virtually no Clq at all; CRP trimers also bound to fluid phase Clq. Binding was Ca<sup>2+</sup> independent and increased as the ionic strength or pH were lowered, characteristics comparable to binding of aggregated IgG to Clq; it was not inhibited by phosphorylcholine. CRP trimers consumed total C, C1 and C2 hemolytic activities upon incubation in fresh human serum, but much less efficiently than did CRP-protamine complexes or aggregated IgG. CRP trimers failed to deplete alternative C pathway hemolytic activity at all. The stable, chem. defined CRP oligomers described in this report, which bind Clq efficiently but display poor ability to activate the classical C pathway in the absence of an appropriate ligand, should be valuable in further studies of the interactions between CRP and the C system.

AB Chem. cross-linked C-reactive protein (CRP) oligomers were prepd. and characterized, and Clq binding and complement (C) activation were investigated. Purified human CRP was polymd. in the presence of both non-cleavable and cleavable crosslinking agents and further sepd. by Superose 12 anal. FPLC column chromatog. into fractions of 110 KDa (**pentameric** monomers), 220 KDa (dimers) and 330 KDa (trimers); virtually no larger oligomers were formed under a variety of exptl. conditions. CRP subunits were cross-linked both within and between CRP **pentamers**. CRP trimers retained native CRP antigenicity without expression of neo-CRP epitopes. CRP trimers showed maximal binding and CRP dimers showed partial binding of solid phase Clq while CRP monomers bound virtually no Clq at all; CRP trimers also bound to fluid phase Clq. Binding was Ca<sup>2+</sup> independent and increased as the ionic strength or pH were lowered, characteristics comparable to binding of aggregated IgG to Clq; it was not inhibited by phosphorylcholine. CRP trimers consumed total C, C1 and C2 hemolytic activities upon incubation in fresh human serum, but much less efficiently than did CRP-protamine complexes or aggregated IgG. CRP trimers failed to deplete alternative C pathway hemolytic activity at all. The stable, chem. defined CRP oligomers described in this report, which bind Clq efficiently but display poor ability to activate the classical C pathway in the absence of an appropriate ligand, should be valuable in further studies of the interactions between CRP and the C system.

IT 81069-02-5 82436-77-9

RL: BIOL (Biological study)

(C-reactive **protein oligomerization** by, human classical complement pathway activation in relation to)

AN 1988:626424 CAPLUS

DN 109:226424

TI Coordinated assembly of multisubunit **proteins:****oligomerization** of bacterial enterotoxins in vivo and in vitro

AU Hardy, Simon J. S.; Holmgren, Jan; Johansson, Susanne; Sanchez, Joaquin; Hirst, Timothy R.

CS Dep. Biol., Univ. York, York, YO1 5DD, UK

SO Proc. Natl. Acad. Sci. U. S. A. (1988), 85(19), 7109-13

CODEN: PNASA6; ISSN: 0027-8424

DT Journal

LA English

AB The assembly, in vivo and in vitro, of a family of hexameric, heat-labile enterotoxins produced by diarrheagenic bacteria was studied. The toxins, which consist of an A subunit and 5 B subunits, are assembled by a highly coordinated process that ensures secretion of the holotoxin complex. It was shown that (1) oxidn. of cysteine residues in the B subunits is a prerequisite step in vivo formation of B-subunit **pentamers**, (2) redn. of dissocd. B subunits in vitro abolishes their ability to reassemble, (3) the kinetics of B-**pentamer** assembly in vivo can be mimicked under defined conditions in vitro, (4) A subunits cannot assoc. with fully assembled B **pentamers** in vitro, and (5) A subunits cause an .apprx.3-fold acceleration in the rate of B-subunit **pentamerization** in vivo, implying that A subunits play a coordinating role in the pathway of holotoxin assembly. The last finding is likely to be of general significance, since it provides a mechanism

for preferentially excluding or favoring certain intermediates in the assembly of multisubunit proteins.

TI Coordinated assembly of multisubunit **proteins:****oligomerization** of bacterial enterotoxins in vivo and in vitro

AB The assembly, in vivo and in vitro, of a family of hexameric, heat-labile enterotoxins produced by diarrheagenic bacteria was studied. The toxins, which consist of an A subunit and 5 B subunits, are assembled by a highly coordinated process that ensures secretion of the holotoxin complex. It was shown that (1) oxidn. of cysteine residues in the B subunits is a prerequisite step in vivo formation of B-subunit **pentamers**, (2) redn. of dissocd. B subunits in vitro abolishes their ability to reassemble, (3) the kinetics of B-**pentamer** assembly in vivo can be mimicked under defined conditions in vitro, (4) A subunits cannot assoc. with fully assembled B **pentamers** in vitro, and (5) A subunits cause an .apprx.3-fold acceleration in the rate of B-subunit **pentamerization** in vivo, implying that A subunits play a coordinating role in the pathway of holotoxin assembly. The last finding is likely to be of general significance, since it provides a mechanism

for preferentially excluding or favoring certain intermediates in the assembly of multisubunit proteins.

Chemical Genes S D + F (P. 13)

Ant of Schell (P 10) bear P13

Slavin -

272; 624-626

Red + bodies with

1978, 1978,

Did not evaluate  
person's genetic  
information  
p. 13

The receptor only

Pat-F proteins p. 4  
is a whole → bear  
inhibit

1994 - FERS Letters, 34, 54-58

BCL1

low.

if they

Nature, 1993, 363: 446-448

S + F - Hinge Region

Thrombocytopenia 4

Substrate  
Anti-ID 9-10  
Anti-B1-antigen #6  
opposite to

S-D-F

Third of them  
made 3 of them  
S + F are expressed at high level

S = 85 KDA  
F = 90 + 180